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Total Number of Pages in This Submission

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Application Number

10/629,448

Filing Date

July 29, 2003

First Named Inventor

Kelkar et. al.

Art Unit

1631

Examiner Name

Loria Clow

Attorney Docket Number

CHA9 2003 0003 US1

**ENCLOSURES (Check all that apply)**☐

Fee Transmittal Form

☐

Fee Attached

☐

Amendment/Reply

☐

After Final

☐

Affidavits/declaration(s)

☐

Extension of Time Request

☐

Express Abandonment Request

☐

Information Disclosure Statement

☐

Certified Copy of Priority Document(s)

☐Reply to Missing Parts/  
Incomplete Application☐Reply to Missing Parts  
under 37 CFR 1.52 or 1.53☐

Drawing(s)

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☐Petition to Convert to a  
Provisional Application☐Power of Attorney, Revocation  
Change of Correspondence Address☐

Terminal Disclaimer

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Request for Refund

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After Allowance Communication to TC

☐Appeal Communication to Board  
of Appeals and Interferences☐Appeal Communication to TC  
(Appeal Notice, Brief, Reply Brief)☐

Proprietary Information

☐

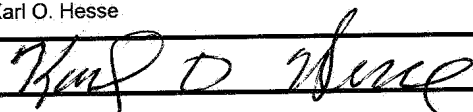
Status Letter

☒Other Enclosure(s) (please identify  
below):Resubmission of Appeal Brief previously filed  
on October 3, 2007.**Remarks**It is believed that no additional fees are due at this time, however, in the event that an additional  
fee is required, please charge that fee to deposit account number 09-0469.**SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT**

Firm Name

Karl O. Hesse

Signature



Printed name

Karl O. Hesse

Date

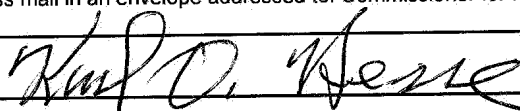
November 7, 2007

Reg. No.

25,398

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This collection of information is required by 37 CFR 1.5. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.11 and 1.14. This collection is estimated to 2 hours to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. **SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.**

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1           **IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

2  
3     Date:       November 7, 2007

4  
5     In re application of:

6     **Kelkar et al**

7     Serial No.: 10/629,448

8     Filed: July 29, 2003

9     Group Art Unit: 1631

10    Examiner: **Loria Clow**

11    FOR: **Method and Program**

12    **Product for Discovering**

13    **Similar Gene Expression Profiles**

I hereby certify that this correspondence is being EFS-Web  
or facsimile transmitted to the United States Patent and  
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on: NOV 7, 2007 by: KARL O MESSE

Karl O Messe

Signature

NOV. 7, 2007

Date of Signature

14  
15  
16           **AMENDED APPEAL BRIEF IN SUPPORT OF APPEAL FROM**  
17           **THE PRIMARY EXAMINER TO THE BOARD OF APPEALS**

18  
19     Assistant Commissioner for Patents

20     Washington DC 20231

21  
22     Sir:

23  
24           Appellants herewith submit an Amended Appeal Brief in  
25     support of the appeal to the Board of Patent Appeals and  
26     Interferences from the decision dated May 16, 2007 of the Primary  
27     Examiner finally rejecting claims 1-6, 10-16 and 20.

1           **(I) Real Party in Interest**

2           The real party in interest in this appeal is International  
3 Business Machines Corporation, a New York corporation, assignee  
4 of the entire right, title and interest in the claimed invention.  
5

6           **(II) Related Appeals and Interferences**

7           No other appeals or interferences are known to the  
8 Appellants, the Appellants' legal representative, or assignee  
9 that will directly affect or be directly affected by or have a  
10 bearing on the Board's decision in this appeal.  
11

12           **(III) Status of Claims**

13           Claims 1-6, 10-16 and 20 are pending in this application.  
14           Claims 7-9 and 17-19 were canceled after restriction.  
15           The rejection of claims 10-16 and 20 under 35 U.S.C. 101 and  
16           the rejection of claims 1-6 under 35 U.S.C. 101 and  
17           for new matter is appealed.  
18

19           When this application was filed in 2003, applicants'  
20 attorney believed that providing independent claims would  
21 facilitate prosecution because they could be allowed or rejected  
22 without requiring rewriting to incorporate independent claim  
23 limitations into dependent claims when they were found to be  
24 allowable. It is understood that currently this practice is not  
25 permitted in excess of four claims and applicants' attorney  
26 regrets any inconvenience caused thereby.  
27

28           **(IV) Status of Amendments**

29           The amendment filed before final has been entered.  
30           The amendment filed after final has not been entered.  
31

1            (V) Summary of Claimed Subject Matter

2  
3            References to paragraphs are made to the application as  
4 published.

5  
6            1. A method for determining similarity between portions of gene  
7 expression profiles in a computer comprising the steps of:

8            processing a number of gene expression profiles with a similar  
9 sequences algorithm that is a time and intensity invariant  
10 correlation function to obtain a data set of gene expression profile  
11 pairs and a match fraction for each gene expression profile pair;

12 **Page 7, Line 31-Page 8, Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

13            listing gene expression profile pairs in clusters by their  
14 match fractions; **Page 8 Lines 16-26 (paragraph 38) and Fig. 2 # 223**

15            removing a first gene expression profile from a cluster when  
16 another cluster has another gene expression profile with a higher  
17 match fraction with the first gene expression profile, unless the  
18 another gene expression profile requires a larger number of  
19 subsequences to achieve similarity with the first gene expression  
20 profile; **Page 8 Line 27-Page 9 Line 7 (paragraph 39) and Fig. 2 #**

21 **225**

22            repeating the removing step until all gene expression profiles  
23 are listed in only one cluster; **Page 8 Line 27-Page 9 Line 7**

24 **(Paragraph 39) last sentence**

25            providing output of the listing of clusters of gene  
26 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**

27 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**

1        2. A method for determining similarity between portions of gene  
2 expression profiles comprising the steps of:

3        processing a number of gene expression profiles with a similar  
4 sequences algorithm that is a time and intensity invariant  
5 correlation function to obtain a data set of gene expression pairs  
6 and a match fraction for each pair; **Page 7,Line 31 - Page 8,Line 9**  
7 **(Paragraph 36) and Fig. 1, # 213, 215)**

8        listing gene expression pairs in clusters by their match  
9 fractions; **Page 8 Lines 16-26 (Paragraph 38) and Fig.2 # 223**

10       removing a first gene from a first cluster when the first gene  
11 is also in a second cluster which has another gene with a higher  
12 match fraction with the first gene than any of the genes in the  
13 first cluster have with the first gene, but; **Page 8 Line 27 - Page 9**  
14 **Line 7 (Paragraph 39) and Fig. 2 # 225**

15       retaining the first gene in the first cluster and removing the  
16 first gene from the second cluster when the difference between the  
17 highest match fraction of the first gene with a gene in the first  
18 cluster and the highest match fraction of the first gene with a gene  
19 in the second cluster is less than a minimum difference threshold  
20 and the number of subsequences represented in the similar gene pair  
21 having the highest match fraction in the first cluster is higher  
22 than the number of subsequences represented in the similar gene pair  
23 having the highest match fraction in the second cluster; **Page 9 Line**  
24 **18 - Page 10 Line 10 (Paragraphs 41, 42, 43 and 56) and Fig. 2 # 225**

25       repeating the removing step until all genes are listed in only  
26 one cluster; **Page 8 Line 27 - Page 9 Line 7 (Paragraph 39) last**  
27 **sentence**

28       providing output of the listing of clusters of gene  
29 expression profiles. **Page 6 Lines 24 - 31 and Page 7 Lines 19-24**  
30 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**

1        3. A method of determining similarity between portions of gene  
2 expression profiles comprising the steps of:

3        processing data embodying a number of gene expression profiles  
4 with a similar sequences algorithm in a computer that is a time and  
5 intensity invariant correlation function to obtain a data set of  
6 gene expression pairs and a match fraction for each pair; **Page**

7 **7,Line 31 - Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

8        choosing a threshold match fraction; **Page 13 Lines 6-20**

9 **(Paragraph 52) sentence 6 and Fig.2 # 217**

10        listing gene expression pairs in clusters by their match  
11 fractions above the threshold; **Page 13 Lines 15-20 (Paragraph 52)**  
12 **and Fig.2 #s 221, 215, 219 and 223**

13        adding each gene not already in a cluster to a cluster having  
14 another gene having a highest match fraction with the each gene  
15 without regard of the threshold; **Page 9 Lines 8-14 (Paragraph 40)**  
16 **and Fig 2 # 229**

17        removing a first gene from a cluster when the first gene is  
18 also in another cluster which has another gene with a higher match  
19 fraction with the first gene than any of the genes in the cluster  
20 have with the first gene; **Page 8 Line 27-Page 9 Line 7 (Paragraph**  
21 **39) first sentence and Fig. 2 # 225**

22        repeating the removing step until all genes are listed in only  
23 one cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph 39) last**  
24 **sentence**

25        providing output of the listing of clusters of gene  
26 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**  
27 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**

1        4. A method for determining similarity between portions of gene  
2 expression profiles comprising the steps of:

3        processing a number of gene expression profiles with a similar  
4 sequences algorithm that is a time and intensity invariant  
5 correlation function with a computer to obtain a data set of gene  
6 expression pairs and a match fraction for each pair; **Page 7, Line 31-**  
7 **Page 8, Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

8        choosing a threshold match fraction; **Page 13 Lines 5-20**  
9 **(Paragraph 52) sentence 6 and Fig.2 # 217**

10        listing gene expression pairs in clusters by their match  
11 fractions above the threshold; **Page 8 Lines 16-26 (paragraph 38) and**  
12 **Fig.2 # 223**

13        adding each gene not already in a cluster to a cluster having  
14 another gene having a highest match fraction disregarding the  
15 threshold with the each gene; **Page 9 Lines 8-14 (Paragraph 40) and**  
16 **Fig 2 # 229**

17        removing a first gene from a first cluster when the first gene  
18 is also in a second cluster which has another gene with a higher  
19 match fraction with the first gene than any of the genes in the  
20 first cluster have with the first gene, **Page 8 Line 27-Page 9 Line 7**  
21 **(Paragraph 39) first sentence and Fig. 2 # 225**

22        but;

23        retaining the first gene in the first cluster and removing the  
24 first gene from the second cluster when the difference between the  
25 highest match fraction of the first gene with a gene in the first  
26 cluster and the highest match fraction of the first gene with a gene  
27 in the second cluster is less than a minimum difference threshold  
28 and the number of subsequences represented in the similar gene pair  
29 having the highest match fraction in the first cluster is higher  
30 than the number of subsequences represented in the similar gene pair

1 having the highest match fraction in the second cluster; **Page 8 Line**  
2 **27-Page 9 Line 7 (Paragraph 39) second sentence and Fig. 2 # 225**

3  
4 repeating the removing and retaining steps until all genes are  
5 listed in only one cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph**  
6 **39) last sentence**

7 providing output of the listing of clusters of gene  
8 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**  
9 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**



1           5. A method in a computer for determining similarity between  
2 genes comprising the steps of:

3           listing genes to be compared in a data set by their gene  
4 expression profiles; **Page 7,Line 31-Page 8,Line 9 (Paragraph 36)**  
5 **second sentence and Fig. 1 # 211**

6           processing the listed gene expression profiles with a similar  
7 sequences algorithm that is a time and intensity invariant  
8 correlation function to obtain a data set of gene expression pairs  
9 and a match fraction for each pair; **Page 7,Line 31-Page 8,Line 9**  
10 **(Paragraph 36) and Fig. 1, # 213, 215**

11           choosing a threshold match fraction; **Page 13 Lines 5-20**  
12 **(Paragraph 52) sentence 6 and Fig.2 # 217**

13  
14           creating a set G in which to list indices of genes accounted  
15 for; **Page 8 Lines 11-14 (Paragraph 37) and Fig. 2 # 217**

16           assigning genes i and j to a cluster a if they have a match  
17 fraction greater than the threshold; **Page 8 Lines 16-26 (Paragraph**  
18 **38) second sentence and Fig. 2 # 223 -> ca={i,j,...}**

19           assigning gene k to the cluster a if it has a match fraction  
20 greater than the threshold with either gene i or gene j;  
21 **Page 8 Lines 16-26 (Paragraph 38) last sentence and Fig. 2 # 223 ->**  
22 **ca={i,j,k,...}**

23           assigning genes k and l to a cluster b if they have a match  
24 fraction greater than the threshold and if both gene k and gene l do  
25 not have match fractions above the threshold with either gene i or  
26 gene j;

27 **Page 8 Lines 16-26 (Paragraph 38) and Fig. 2 # 223 -> cb={k,l,...}**

28           repeating the assigning steps until all genes to be compared  
29 have been considered; **Page 13 Lines 5-20 (Paragraph 52) first two**  
30 **sentences and Fig #s 217, 219, and 229**

1 removing a first gene from a cluster when another cluster has  
2 another gene with a higher match fraction with the first gene; **Page**  
3 **8 Line 27-Page 9 Line 7 (Paragraph 39) second sentence and Fig. 2 #**  
4 **225**

5 repeating the removing step until all genes are listed in only  
6 one cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph 39) last**  
7 **sentence**

8 providing output of the listing of clusters of gene  
9 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**  
10 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**

1           6. A method in a computer for determining similarity between  
2 genes comprising the steps of:

3           listing genes to be compared in a data set by their gene  
4 expression profiles; **Page 7,Line 31-Page 8,Line 9 (Paragraph 36)**  
5 **second sentence and Fig. 1 # 211**

6           processing the listed gene expression profiles with a similar  
7 sequences algorithm that is a time and intensity invariant  
8 correlation function to obtain a data set of gene expression pairs  
9 and a match fraction for each pair; **Page 7,Line 31-Page 8,Line 9**  
10 **(Paragraph 36) and Fig. 1, # 213, 215**

11           choosing a threshold match fraction; **Page 13 Lines 5-20**  
12 **(Paragraph 52) sentence 6 and Fig.2 # 217**

13           creating a set G in which to list indices of genes accounted  
14 for; **Page 13 Lines 5-20 (Paragraph 52) 3rd and 4th sentences and**  
15 **Fig. 2 # 217**

16           assigning genes i and j to cluster 1 if they have a match  
17 fraction greater than the threshold; **Page 13 Line 21-Page 14 Line 6**  
18 **and Page 14 Lines 8-12 (Paragraphs 53 and 54) first sentence and**  
19 **Table IV**

20           assigning gene k to cluster 1 if it has a match fraction  
21 greater than the threshold with either gene i or gene j; **Page 13**  
22 **Line 21-Page 14 Line 6, Page 14 Lines 8-12, Page 14 Line 24-Page 15**  
23 **Line 3 (Paragraphs 53, 54 2nd sentence, 56) and Table IV**

24           assigning genes k and l to cluster 2 if they have a match  
25 fraction greater than the threshold and if both gene k and gene l do  
26 not have match fractions above the threshold with either gene i or  
27 gene j; **Page 13 Line 21-Page 14 Line 6, Page 14 Lines 8-12, Page 14**  
28 **Line 24-Page 15 Line 3 (Paragraphs 53, 54 2nd sentence, 56) and**  
29 **Table IV and Fig. 2 # 225**

30           removing a first gene from a cluster when another cluster has  
31 another gene with a higher match fraction with the first gene,

1 unless the another gene requires a larger number of subsequences to  
2 achieve similarity with the first gene; **Page 14 Line 24 - Page 15**  
3 **Line 3 (Paragraph 56) beginning at the 3rd sentence and Fig. 2 # 225**  
4 repeating the removing step until all genes are listed in only  
5 one cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph 39) last**  
6 **sentence**  
7 providing output of the listing of clusters of gene  
8 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**  
9 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**  
10  
11

1        10. A program product having computer readable code stored on a  
2        recordable media for determining similarity between portions of gene  
3        expression profiles comprising:

4        programmed means for processing a number of gene expression  
5        profiles with a similar sequences algorithm that is a time and  
6        intensity invariant correlation function to obtain a data set of  
7        gene expression pairs and a match fraction for each pair;

8        **Page 7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

9        programmed means for listing gene expression pairs in clusters  
10       by their match fractions; **Page 8 Lines 16-26 (paragraph 38) and**  
11       **Fig.2 # 223**

12       programmed means for removing a first gene from a cluster when  
13       the first gene is also in another cluster which has another gene  
14       with a higher match fraction with the first gene than any of the  
15       genes in the cluster have with the first gene; **Page 8 Line 27-Page 9**  
16       **Line 7 (paragraph 39) and Fig. 2 # 225**

17       programmed means for repeating the removing step until all  
18       genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
19       **(Paragraph 39) last sentence**

1        11. A program product having computer readable code stored on a  
2 recordable media for determining similarity between portions of gene  
3 expression profiles using output from a similar sequences algorithm  
4 that is a time and intensity invariant correlation function  
5 comprising:

6        programmed means for providing a gene expression profile data  
7 set as input to programmed means embodying a similar sequences  
8 algorithm that is a time and intensity invariant correlation  
9 function to obtain a data set of gene expression pairs and a match  
10 fraction for each pair as output from the programmed means embodying  
11 a similar sequences algorithm; **Page 7,Line 31-Page 8,Line 9; Page**  
12 **10, Line 22-Page 11,Line 7 (Paragraphs 36, 44) and Fig. 1, # 213,**  
13 **215)**

14        programmed means for listing the gene expression pairs in  
15 clusters by their match fractions; **Page 7,Line 31-Page 8,Line 9**  
16 **(Paragraph 36) beginning at the second sentence and Fig. 1 # 215**  
17

18        programmed means for removing a first gene from a cluster when  
19 the first gene is also in another cluster which has another gene  
20 with a higher match fraction with the first gene than any of the  
21 genes in the cluster have with the first gene; **Page 8 Line 27-Page 9**  
22 **Line 7 (Paragraph 39) first sentence and Fig. 2 # 225**

23        programmed means for repeating the removing step until all  
24 genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
25 **(Paragraph 39) last sentence**

1 12. A program product having computer readable code stored on a  
2 recordable media for determining similarity between portions of gene  
3 expression profiles comprising the steps of:

4 programmed means for processing a number of gene expression  
5 profiles with a similar sequences algorithm that is a time and  
6 intensity invariant correlation function to obtain a data set of  
7 gene expression pairs and a match fraction for each pair; **Page**  
8 **7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

9 programmed means for listing gene expression pairs in clusters  
10 by their match fractions; **Page 8 Lines 16-26 (paragraph 38) and**  
11 **Fig.2 # 223**

12 programmed means for removing a first gene from a first cluster  
13 when the first gene is also in a second cluster which has another  
14 gene with a higher match fraction with the first gene than any of  
15 the genes in the first cluster have with the first gene, **Page 8 Line**  
16 **27-Page 9 Line 7 (Paragraph 39) first sentence and Fig. 2 # 225**  
17 but;

18 programmed means for retaining the first gene in the first  
19 cluster and removing the first gene from the second cluster when the  
20 difference between the highest match fraction of the first gene with  
21 a gene in the first cluster and the highest match fraction of the  
22 first gene with a gene in the second cluster is less than a minimum  
23 difference threshold and the number of subsequences represented in  
24 the similar gene pair having the highest match fraction in the first  
25 cluster is higher than the number of subsequences represented in the  
26 similar gene pair having the highest match fraction in the second  
27 cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph 39) second sentence**  
28 **and Fig. 2 # 225**

29 programmed means for repeating the removing step until all  
30 genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
31 **(Paragraph 39) last sentence**

1        13. A program product having computer readable code stored on a  
2        recordable media for determining similarity between portions of gene  
3        expression profiles comprising the steps of:

4        programmed means for processing a number of gene expression  
5        profiles with a similar sequences algorithm that is a time and  
6        intensity invariant correlation function to obtain a data set of  
7        gene expression pairs and a match fraction for each pair; **Page**  
8        **7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

9        programmed means for choosing a threshold match fraction; **Page**  
10       **13 Lines 6-20 (Paragraph 52) sentence 6 and Fig.2 # 217**

11       programmed means for listing gene expression pairs in clusters  
12       by their match fractions above the threshold; **Page 8 Lines 16-26**  
13       **(paragraph 38) and Fig.2 # 223**

14       programmed means for adding each gene not already in a cluster  
15       to a cluster having another gene having a highest match fraction  
16       with the each gene without regard of the threshold; **Page 9 Lines 8-**  
17       **14 (Paragraph 40) and Fig 2 # 229**

18       programmed means for removing a first gene from a cluster when  
19       the first gene is also in another cluster which has another gene  
20       with a higher match fraction with the first gene than any of the  
21       genes in the cluster have with the first gene; **Page 8 Line 27-Page 9**  
22       **Line 7 (Paragraph 39) first sentence and Fig. 2 # 225**

23       programmed means for repeating the removing step until all  
24       genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
25       **(Paragraph 39) last sentence**



1 14. A program product having computer readable code stored on a  
2 recordable media for determining similarity between portions of gene  
3 expression profiles comprising the steps of:

4 programmed means for processing a number of gene expression  
5 profiles with a similar sequences algorithm that is a time and  
6 intensity invariant correlation function to obtain a data set of  
7 gene expression pairs and a match fraction for each pair; **Page**

8 **7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

9 programmed means for choosing a threshold match fraction; **Page**  
10 **13 Lines 6-20 (Paragraph 52) sentence 6 and Fig.2 # 217**

11 programmed means for listing gene expression pairs in clusters  
12 by their match fractions above the threshold; **Page 8 Lines 16-26**  
13 **(paragraph 38) and Fig.2 # 223**

14 programmed means for adding each gene not already in a cluster  
15 to a cluster having another gene having a highest match fraction  
16 disregarding the threshold with the each gene; **Page 9 Lines 8-14**  
17 **(Paragraph 40) and Fig 2 # 229**

18 programmed means for removing a first gene from a first cluster  
19 when the first gene is also in a second cluster which has another  
20 gene with a higher match fraction with the first gene than any of  
21 the genes in the first cluster have with the first gene, **Page 8 Line**  
22 **27-Page 9 Line 7 (Paragraph 39) first sentence and Fig. 2 # 225**

23 but;

24 programmed means for retaining the first gene in the first  
25 cluster and removing the first gene from the second cluster when the  
26 difference between the highest match fraction of the first gene with  
27 a gene in the first cluster and the highest match fraction of the  
28 first gene with a gene in the second cluster is less than a minimum  
29 difference threshold and the number of subsequences represented in  
30 the similar gene pair having the highest match fraction in the first  
31 cluster is higher than the number of subsequences represented in the

1 similar gene pair having the highest match fraction in the second  
2 cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph 39) second sentence**  
3 **and Fig. 2 # 225**

4 programmed means for repeating the removing and retaining steps  
5 until all genes are listed in only one cluster. **Page 8 Line 27-Page**  
6 **9 Line 7 (Paragraph 39) last sentence**

1        15. A program product having computer readable code stored on a  
2 recordable media for determining similarity between genes comprising  
3 the steps of:

4        programmed means for listing genes to be compared by their gene  
5 expression profiles; **Page 7,Line 31-Page 8,Line 9 (Paragraph 36)**  
6 **second sentence and Fig. 1 # 211**

7        programmed means for processing the listed gene expression  
8 profiles with a similar sequences algorithm that is a time and  
9 intensity invariant correlation function to obtain a data set of  
10 gene expression pairs and a match fraction for each pair; **Page**  
11 **7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

12        programmed means for choosing a threshold match fraction; **Page**  
13 **13 Lines 6-20 (Paragraph 52) sentence 6 and Fig.2 # 217**

14        programmed means for creating a null set  $G(0)$  to hold genes  
15 accounted for; **Page 13 Lines 6-20 (Paragraph 52) 3rd and 4th**  
16 **sentences and Fig. 2 # 217**

17        programmed means for assigning genes  $i$  and  $j$  to cluster 1 if  
18 they have a match fraction greater than the threshold; **Page 13 Line**  
19 **21-Page 14 Line 6 and Page 14 Lines 8-12 (Paragraphs 53 and 54)**  
20 **first sentence and Table IV**

21        programmed means for assigning gene  $k$  to cluster 1 if it has a  
22 match fraction greater than the threshold with either gene  $i$  or gene  
23  $j$ ; **Page 13 Line 21-Page 14 Line 6, Page 14 Lines 8-12, Page 14 Line**  
24 **24-Page 15 Line 3 (Paragraphs 53, 54 2nd sentence, 56) and Table IV**

25        programmed means for assigning genes  $k$  and  $l$  to cluster 2 if  
26 they have a match fraction greater than the threshold and if both  
27 gene  $k$  and gene  $l$  do not have match fractions above the threshold  
28 with either gene  $i$  or gene  $j$ ; **Page 13 Line 21-Page 14 Line 6, Page**  
29 **14 Lines 8-12, Page 14 Line 24-Page 15 Line 3 (Paragraphs 53, 54 2nd**  
30 **sentence, 56) and Table IV and Fig. 2 # 225**

1       programmed means for removing a first gene from a cluster when  
2 another cluster has another gene with a higher match fraction with  
3 the first gene; **Page 14 Line 24 - Page 15 Line 3 (Paragraph 56)**  
4 **beginning at the 3rd sentence and Fig. 2 # 225**

5       programmed means for repeating the removing step until all  
6 genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
7 **(Paragraph 39) last sentence**

1        16. A program product having computer readable code stored on a  
2 recordable media for determining similarity between genes comprising  
3 the steps of:

4        programmed means for listing genes to be compared by their gene  
5 expression profiles; **Page 7,Line 31-Page 8,Line 9 (Paragraph 36)**  
6 **second sentence and Fig. 1 # 211**

7        programmed means for processing the listed gene expression  
8 profiles with a similar sequences algorithm that is a time and  
9 intensity invariant correlation function to obtain a data set of  
10 gene expression pairs and a match fraction for each pair; **Page**  
11 **7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

12        programmed means for choosing a threshold match fraction; **Page**  
13 **13 Lines 5-20 (Paragraph 52) sentence 6 and Fig.2 # 217**

14        programmed means for creating a null set  $G(0)$  to hold genes  
15 accounted for; **Page 8 Lines 11-14 (Paragraph 37 and Fig. 2 # 217**

16        programmed means for assigning genes  $i$  and  $j$  to cluster 1 if  
17 they have a match fraction greater than the threshold; **Page 13 Line**  
18 **21-Page 14 Line 6 and Page 14 Lines 8-12 (Paragraphs 53 and 54)**  
19 **first sentence and Table IV**

20        programmed means for assigning gene  $k$  to cluster 1 if it has a  
21 match fraction greater than the threshold with either gene  $i$  or gene  
22  $j$ ; **Page 13 Line 21-Page 14 Line 6, Page 14 Lines 8-12, Page 14 Line**  
23 **24-Page 15 Line 3 (Paragraphs 53, 54 2nd sentence, 56) and Table IV**

24        programmed means for assigning genes  $k$  and  $l$  to cluster 2 if  
25 they have a match fraction greater than the threshold and if both  
26 gene  $k$  and gene  $l$  do not have match fractions above the threshold  
27 with either gene  $i$  or gene  $j$ ; **Page 13 Line 21-Page 14 Line 6, Page**  
28 **14 Lines 8-12, Page 14 Line 24-Page 15 Line 3 (Paragraphs 53, 54 2nd**  
29 **sentence, 56) and Table IV and Fig. 2 # 225**

1       programmed means for removing a first gene from a cluster when  
2 another cluster has another gene with a higher match fraction with  
3 the first gene, unless the another gene requires a larger number of  
4 subsequences to achieve similarity with the first gene; **Page 14 Line**  
5 **24 - Page 15 Line 3 (Paragraph 56) beginning at the 3rd sentence and**  
6 **Fig. 2 # 225**

7       programmed means for repeating the removing step until all  
8 genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
9 **(Paragraph 39) last sentence**

1        20. In a method of determining similarity between portions of  
2 gene expression profiles which includes processing a number of gene  
3 expression profiles using a computer with a similar sequences  
4 algorithm that is a time and intensity invariant correlation  
5 function to obtain a data set of gene expression pairs and a match  
6 fraction for each pair, **Page 7, Line 31-Page 8, Line 9 (Paragraph 36**  
7 **and Fig. 1, # 213, 215** the improvement comprising the steps of:

8        listing gene expression pairs in clusters by their match  
9 fractions; **Page 8 Lines 16-26 (paragraph 38) and Fig.2 # 223**

10       removing a first gene from a cluster when another cluster has  
11 another gene with a higher match fraction with the first gene,  
12 unless the another gene requires a larger number of subsequences to  
13 achieve similarity with the first gene; **Page 14 Line 24 - Page 15**  
14 **Line 3 (Paragraph 56) beginning at the 3rd sentence and Fig. 2 # 225**

15       repeating the removing step until all genes are listed in only  
16 one cluster; **Page 8 Line 27-Page 9 Line 7 (Paragraph 39) last**  
17 **sentence**

18       providing output of the listing of clusters of gene  
19 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**  
20 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**

1           **(VI) Grounds of Rejection to be reviewed on Appeal**

2  
3           Claims 1-6, 10-16 and 20 are pending in this application.

4  
5           Claims 7-9 and 17-19 were canceled after restriction.

6  
7           The rejection of claims 10-16 and 20 under 35 U.S.C. 101 and  
8           the rejection of claims 1-6 under 35 U.S.C. 101 and for new matter  
9           is appealed.

10  
11          The issues in this appeal are:

12  
13       I.    Whether output to a user is a required claim step in order to  
14       define an invention, that is a practical application which is  
15       useful, concrete and tangible.

16           Claim 10 is representative of claims 10 - 16 which have been  
17       rejected under 35 U.S.C. 101 and is related to Issue I

18  
19       II.   Whether applicants' teaching of a personal computer with  
20       implicit, intrinsic and inherent output means in the specification  
21       support claims 1 - 6 and 20 without adding new matter.

22           Claim 1 is representative of claims 1 - 6, 20 which have been  
23       rejected as containing new matter and is related to Issue II  
24



1            (VII) Argument

2  
3    **Issue I:** Whether output to a user is a required claim step in order  
4    to define an invention, that is a practical application which is  
5    useful, concrete and tangible.  
6

7            Appellants claim in representative claim 10:

8            10. A program product having computer readable code stored on a  
9    recordable media for determining similarity between portions of gene  
10   expression profiles comprising:

11           programmed means for processing a number of gene expression  
12   profiles with a similar sequences algorithm that is a time and  
13   intensity invariant correlation function to obtain a data set of  
14   gene expression pairs and a match fraction for each pair; **Page**  
15   **7,Line 31-Page 8,Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

16           programmed means for listing gene expression pairs in clusters  
17   by their match fractions; **Page 8 Lines 16-26 (paragraph 38) and**  
18   **Fig.2 # 223**

19           programmed means for removing a first gene from a cluster when  
20   the first gene is also in another cluster which has another gene  
21   with a higher match fraction with the first gene than any of the  
22   genes in the cluster have with the first gene; **Page 8 Line 27-Page 9**  
23   **Line 7 (paragraph 39) and Fig. 2 # 225**

24           programmed means for repeating the removing step until all  
25   genes are listed in only one cluster. **Page 8 Line 27-Page 9 Line 7**  
26   **(Paragraph 39) last sentence**

1 Applicants believe that the specification and claims indeed do  
2 describe a method and a program product that produce a result that  
3 has substantial and credible utility as required by MPEP 2107 II and  
4 that the claims are limited to a narrow practical application in a  
5 computer related art.  
6

7 The Examiner relies on the "New Interim Guidelines" to  
8 interpret the requirements of the Federal Courts under the current  
9 law to require claiming "output to a user". Applicants believe that  
10 the Examiner is mistaken and is applying an interpretation of the  
11 definition of the word tangible that is:

- 12 1) narrower than appropriate under the current law and is
- 13 2) narrower than required under the "New Guidelines".  
14

15 1) The introduction to the "New Guidelines" states:  
16 "These Examination Guidelines ("Guidelines") are based on the USPTO's current understanding of  
17 the law and are believed to be fully consistent with binding precedent of the Supreme Court, the  
18 Federal Circuit and the Federal Circuit's predecessor courts. These Guidelines do not constitute  
19 substantive rulemaking and hence do not have the force and effect of law."  
20

21 In following the "Guidelines", the Examiner appears to require  
22 separate interpretations of the words useful, concrete and tangible.  
23

24 Applicants' attorney has found no basis in any of the Federal  
25 Circuit opinions using these words that imply that these terms are  
26 to have separate meanings. They appear to always be used together  
27 as synonyms for the concept of being useful and non-abstract.  
28 Applicants' attorney has requested that the Examiner provide a  
29 citation to a court's requirement that these terms are part of a  
30 three pronged test if such is the case in order to help applicants

1 decide whether to appeal or request continued examination. No  
2 citation was provided.

3 2) Even under the "Guidelines, the Examiners interpretation of  
4 the word tangible is unnecessarily narrow.

5 The "Guidelines" at page 13 recite

6 "Accordingly, a complete definition of the scope of 35 U.S.C. § 101, reflecting Congressional intent,  
7 is that any new and useful process, machine, manufacture or composition of matter under the sun that  
8 is made by man is the proper subject matter of a patent. The subject matter courts have found to be  
9 outside of, or exceptions to, the four statutory categories of invention is limited to abstract ideas, laws  
10 of nature and natural phenomena. While this is easily stated, determining whether an applicant is  
11 seeking to patent an abstract idea, a law of nature or a natural phenomenon has proven to be  
12 challenging."

13  
14 Beginning at page 21 the "Guidelines" recite:

15 "TANGIBLE RESULT"

16 "The tangible requirement does not necessarily mean that a claim must either be tied to a particular  
17 machine or apparatus or must operate to change articles or materials to a different state or thing.  
18 However, the tangible requirement does require that the claim must recite more than a § 101 judicial  
19 exception, in that the process claim must set forth a practical application of that § 101 judicial exception  
20 to produce a real-world result. Benson, 409 U.S. at 71-72, 175 USPQ at 676-77 (invention ineligible  
21 because had "no substantial practical application."). "[A]n application of a law of nature or mathematical  
22 formula to a ... process may well be deserving of patent protection." Diehr, 450 U.S. at 187, 209 USPQ  
23 at 8 (emphasis added); see also Corning, 56 U.S. (15 How.) at 268, 14 L.Ed. 683 ("It is for the discovery  
24 or invention of some practical method or means of producing a beneficial result or effect, that a patent is  
25 granted ...").

26  
27 In other words, the opposite meaning of "tangible" is "abstract."  
28 The bare conversion of any binary data as in Gottschalk V. Benson or  
29 the bubble sort of any data as in "Warmerdam, 33 F.3d at 1360, 31 USPQ2d at 1759  
30 ("steps of 'locating' a medial axis, and 'creating' a bubble hierarchy ... describe nothing more than the

1 manipulation of basic mathematical constructs, the paradigmatic 'abstract idea'")" recited at  
2 page 14 of the "Guidelines" are examples of the abstract.

3  
4 Applicants' process does not convert or process just any data but is  
5 limited to useful concrete and non-abstract gene expression profiles  
6 in a data base of such profiles. Applicants' process is but one  
7 application of many possible applications of the mathematical steps  
8 involved in obtaining the useful result.

9  
10 At page 17 of the "Guidelines we see:

11 While abstract ideas, natural phenomena, and laws of nature are not eligible for patenting, methods and  
12 products employing abstract ideas, natural phenomena, and laws of nature to perform a real-world  
13 function may well be. In evaluating whether a claim meets the requirements of section 101, the claim  
14 must be considered as a whole to determine whether it is for a particular application of an abstract idea,  
15 natural phenomenon, or law of nature, rather than for the abstract idea, natural phenomenon, or law of  
16 nature itself.

17  
18 As is clear from the specification and the claim limitations,  
19 applicants' process is limited to a particular practical application  
20 and is not an abstract idea, natural phenomenon or a law of nature.

21  
22 The result is that all of the processed gene expression profiles are  
23 each listed in only one cluster. This result of applicants' claims  
24 is a very useful, repeatable and non-abstract result which is  
25 recognized by those skilled in the medical and computer arts to be  
26 of great value and useful, non-abstract and concrete finding of  
27 similar gene expression profiles.

1     **PRIOR ART**

2     Applicants note that their claims have not been rejected on prior  
3     art yet have been restricted on the ground that there were two  
4     groups of claims that required two fields of search. It is not  
5     apparent whether relevant prior art patents were considered by the  
6     Examiner while examining this application. It is believed that the  
7     "Guidelines" on page 10 are helpful in determining both the novelty  
8     of applicants' invention and the **usefulness and non-abstract nature**  
9     of applicants' the invention.

10  
11    As evidenced by the references which applicants have attempted to  
12    incorporate by reference, but have acquiesced to the Examiners  
13    correct requirement to cancel, in addition to applicants teachings  
14    in the background art section of their specification, users in the  
15    medical profession find great value and usefulness in methods for  
16    finding similar gene expression profiles that are tangible and  
17    concrete. See for example US Patent 6,406,853 abstract and claims  
18    25, 26 and US Patent 6,436,642 column 26 beginning at line 15.

19  
20    It is believed that if the rejections under 35 U.S.C. 101 put forth  
21    in this application were appropriate, many of the relevant prior art  
22    patents in the appropriate fields of search would be found to be  
23    invalid. Since they were issued under the guidance of current  
24    statutory law and court cases, it must be that the rejections in  
25    this application are based upon excessively narrow and untenable  
26    interpretation of the current law.

1           **Issue II:** Whether applicants' teaching of a personal computer  
2 with implicit, intrinsic and inherent output means in the  
3 specification support claims 1 - 6 without adding new matter.  
4

5           Appellants claim in representative claim 1:

6           1. A method for determining similarity between portions of gene  
7 expression profiles in a computer comprising the steps of:

8           processing a number of gene expression profiles with a similar  
9 sequences algorithm that is a time and intensity invariant  
10 correlation function to obtain a data set of gene expression profile  
11 pairs and a match fraction for each gene expression profile pair;

12 **Page 7, Line 31-Page 8, Line 9 (Paragraph 36) and Fig. 1, # 213, 215**

13           listing gene expression profile pairs in clusters by their  
14 match fractions; **Page 8 Lines 16-26 (paragraph 38) and Fig. 2 # 223**

15           removing a first gene expression profile from a cluster when  
16 another cluster has another gene expression profile with a higher  
17 match fraction with the first gene expression profile, unless the  
18 another gene expression profile requires a larger number of  
19 subsequences to achieve similarity with the first gene expression  
20 profile; **Page 8 Line 27-Page 9 Line 7 (paragraph 39) and Fig. 2 #**

21 **225**

22           repeating the removing step until all gene expression profiles  
23 are listed in only one cluster; **Page 8 Line 27-Page 9 Line 7**

24 **(Paragraph 39) last sentence**

25           providing output of the listing of clusters of gene  
26 expression profiles. **Page 6 Lines 24-31 and Page 7 Lines 19-24**  
27 **(Paragraphs 32 and 34) and Fig. 8 #s 54 and 66**  
28

1 Applicants' specification recites: The focal point of the  
2 preferred personal computer architecture comprises a processor 51.  
3 The processor 51 is connected to a bus 52 which comprises a set of  
4 data lines, a set of address lines and a set of control lines. A  
5 plurality of I/O devices, memory and storage devices 53-58 and 66  
6 are connected to the bus 52 through separate adapters 59-64 and 67,  
7 respectively. For example, the display 54 may be either a CRT or a  
8 flat panel display.  
9

10 It is believed to be well known in the art as exemplified by  
11 prior art patents that users in the medical profession receive  
12 output from personal computer input/output devices such as  
13 applicants teach in their preferred embodiment. Again, applicants  
14 refer to US Patent 6,406,853 abstract and claims 25, 26 and US  
15 Patent 6,436,642 column 26 beginning at line 15.  
16

17 It is believed that material that is implicit, intrinsic, or  
18 inherent in the application as filed is not new matter.  
19

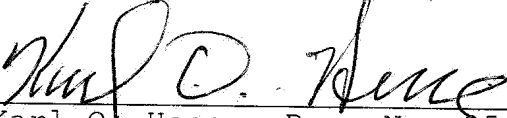
20 In order to be usable by a user, a personal computer  
21 necessarily and constantly exhibits the function of input and  
22 output, and such function was recognized as such by those skilled in  
23 the art of using personal computers. Therefore applicants' addition  
24 of the step of providing such output to satisfy the Examiner's  
25 reading of the guidelines was not new matter but is supported in  
26 their specification by teachings that are implicit, intrinsic and  
27 inherent.  
28

1 Accordingly it is believed that the claims are clear, statutory  
2 and definite and are drawn to a novel and unobvious method and  
3 program product for clustering gene expression profiles which result  
4 is concrete, tangible and directly useful in drug selection and  
5 disease diagnosis.

6  
7 **Request for Relief**  
8

9 Wherefore, Appellants respectfully request that the rejection  
10 of pending claims 1 - 6, 10 - 16 and 20 be reversed.  
11

12 Respectfully submitted,  
13

14   
15 Karl O. Hesse, Reg. No. 25,398  
16 Attorney for Appellants

17 Date: October 3, 2007

18 IBM Corporation  
19 Intellectual Property Law  
20 MG90-201/1  
21 8501 IBM Drive  
22 Charlotte, NC 28262-8563

Land line (704) 895-8241  
Cell phone (704) 724-1413  
Fax: (704) 594-8307



1           **(VIII) Appendix**

2           **Claims Involved in this Appeal**

3  
4           1. A method for determining similarity between portions of gene  
5 expression profiles in a computer comprising the steps of:

6           processing a number of gene expression profiles with a similar  
7 sequences algorithm that is a time and intensity invariant  
8 correlation function to obtain a data set of gene expression profile  
9 pairs and a match fraction for each gene expression profile pair;

10          listing gene expression profile pairs in clusters by their  
11 match fractions;

12          removing a first gene expression profile from a cluster when  
13 another cluster has another gene expression profile with a higher  
14 match fraction with the first gene expression profile, unless the  
15 another gene expression profile requires a larger number of  
16 subsequences to achieve similarity with the first gene expression  
17 profile;

18          repeating the removing step until all gene expression profiles  
19 are listed in only one cluster;

20          providing output of the listing of clusters of gene  
21 expression profiles.  
22

1           2. A method for determining similarity between portions of gene  
2 expression profiles comprising the steps of:

3           processing a number of gene expression profiles with a similar  
4 sequences algorithm that is a time and intensity invariant  
5 correlation function to obtain a data set of gene expression pairs  
6 and a match fraction for each pair;

7           listing gene expression pairs in clusters by their match  
8 fractions;

9           removing a first gene from a first cluster when the first gene  
10 is also in a second cluster which has another gene with a higher  
11 match fraction with the first gene than any of the genes in the  
12 first cluster have with the first gene, but;

13          retaining the first gene in the first cluster and removing the  
14 first gene from the second cluster when the difference between the  
15 highest match fraction of the first gene with a gene in the first  
16 cluster and the highest match fraction of the first gene with a gene  
17 in the second cluster is less than a minimum difference threshold  
18 and the number of subsequences represented in the similar gene pair  
19 having the highest match fraction in the first cluster is higher  
20 than the number of subsequences represented in the similar gene pair  
21 having the highest match fraction in the second cluster;

22          repeating the removing step until all genes are listed in only  
23 one cluster;

24          providing output of the listing of clusters of gene  
25 expression profiles.

1           3. A method of determining similarity between portions of gene  
2 expression profiles comprising the steps of:  
3           processing data embodying a number of gene expression profiles  
4 with a similar sequences algorithm in a computer that is a time and  
5 intensity invariant correlation function to obtain a data set of  
6 gene expression pairs and a match fraction for each pair;  
7           choosing a threshold match fraction;  
8           listing gene expression pairs in clusters by their match  
9 fractions above the threshold;  
10          adding each gene not already in a cluster to a cluster having  
11 another gene having a highest match fraction with the each gene  
12 without regard of the threshold;  
13          removing a first gene from a cluster when the first gene is  
14 also in another cluster which has another gene with a higher match  
15 fraction with the first gene than any of the genes in the cluster  
16 have with the first gene;  
17          repeating the removing step until all genes are listed in only  
18 one cluster;  
19          providing output of the listing of clusters of gene  
20 expression profiles.

1        4. A method for determining similarity between portions of gene  
2 expression profiles comprising the steps of:

3        processing a number of gene expression profiles with a similar  
4 sequences algorithm that is a time and intensity invariant  
5 correlation function with a computer to obtain a data set of gene  
6 expression pairs and a match fraction for each pair;

7        choosing a threshold match fraction;

8        listing gene expression pairs in clusters by their match  
9 fractions above the threshold;

10       adding each gene not already in a cluster to a cluster having  
11 another gene having a highest match fraction disregarding the  
12 threshold with the each gene;

13       removing a first gene from a first cluster when the first gene  
14 is also in a second cluster which has another gene with a higher  
15 match fraction with the first gene than any of the genes in the  
16 first cluster have with the first gene, but;

17       retaining the first gene in the first cluster and removing the  
18 first gene from the second cluster when the difference between the  
19 highest match fraction of the first gene with a gene in the first  
20 cluster and the highest match fraction of the first gene with a gene  
21 in the second cluster is less than a minimum difference threshold  
22 and the number of subsequences represented in the similar gene pair  
23 having the highest match fraction in the first cluster is higher  
24 than the number of subsequences represented in the similar gene pair  
25 having the highest match fraction in the second cluster;

26       repeating the removing and retaining steps until all genes are  
27 listed in only one cluster;

28       providing output of the listing of clusters of gene  
29 expression profiles.

1           5. A method in a computer for determining similarity between  
2 genes comprising the steps of:  
3           listing genes to be compared in a data set by their gene  
4 expression profiles;  
5           processing the listed gene expression profiles with a similar  
6 sequences algorithm that is a time and intensity invariant  
7 correlation function to obtain a data set of gene expression pairs  
8 and a match fraction for each pair;  
9           choosing a threshold match fraction;  
10          creating a set G in which to list indices of genes accounted  
11 for;  
12          assigning genes i and j to a cluster a if they have a match  
13 fraction greater than the threshold;  
14          assigning gene k to the cluster a if it has a match fraction  
15 greater than the threshold with either gene i or gene j;  
16          assigning genes k and l to a cluster b if they have a match  
17 fraction greater than the threshold and if both gene k and gene l do  
18 not have match fractions above the threshold with either gene i or  
19 gene j;  
20          repeating the assigning steps until all genes to be compared  
21 have been considered;  
22          removing a first gene from a cluster when another cluster has  
23 another gene with a higher match fraction with the first gene;  
24          repeating the removing step until all genes are listed in only  
25 one cluster;  
26          providing output of the listing of clusters of gene  
27 expression profiles.  
28

1           6. A method in a computer for determining similarity between  
2 genes comprising the steps of:  
3           listing genes to be compared in a data set by their gene  
4 expression profiles;  
5           processing the listed gene expression profiles with a similar  
6 sequences algorithm that is a time and intensity invariant  
7 correlation function to obtain a data set of gene expression pairs  
8 and a match fraction for each pair;  
9           choosing a threshold match fraction;  
10          creating a set G in which to list indices of genes accounted  
11 for;  
12          assigning genes i and j to cluster 1 if they have a match  
13 fraction greater than the threshold;  
14          assigning gene k to cluster 1 if it has a match fraction  
15 greater than the threshold with either gene i or gene j;  
16          assigning genes k and l to cluster 2 if they have a match  
17 fraction greater than the threshold and if both gene k and gene l do  
18 not have match fractions above the threshold with either gene i or  
19 gene j;  
20          removing a first gene from a cluster when another cluster has  
21 another gene with a higher match fraction with the first gene,  
22 unless the another gene requires a larger number of subsequences to  
23 achieve similarity with the first gene;  
24          repeating the removing step until all genes are listed in only  
25 one cluster;  
26          providing output of the listing of clusters of gene  
27 expression profiles.  
28

1        10. A program product having computer readable code stored on a  
2        recordable media for determining similarity between portions of gene  
3        expression profiles comprising:

4               programmed means for processing a number of gene expression  
5        profiles with a similar sequences algorithm that is a time and  
6        intensity invariant correlation function to obtain a data set of  
7        gene expression pairs and a match fraction for each pair;

8               programmed means for listing gene expression pairs in clusters  
9        by their match fractions;

10               programmed means for removing a first gene from a cluster when  
11        the first gene is also in another cluster which has another gene  
12        with a higher match fraction with the first gene than any of the  
13        genes in the cluster have with the first gene;

14               programmed means for repeating the removing step until all  
15        genes are listed in only one cluster.

1        11. A program product having computer readable code stored on a  
2 recordable media for determining similarity between portions of gene  
3 expression profiles using output from a similar sequences algorithm  
4 that is a time and intensity invariant correlation function  
5 comprising:

6        programmed means for providing a gene expression profile data  
7 set as input to programmed means embodying a similar sequences  
8 algorithm that is a time and intensity invariant correlation  
9 function to obtain a data set of gene expression pairs and a match  
10 fraction for each pair as output from the programmed means embodying  
11 a similar sequences algorithm;

12        programmed means for listing the gene expression pairs in  
13 clusters by their match fractions;

14        programmed means for removing a first gene from a cluster when  
15 the first gene is also in another cluster which has another gene  
16 with a higher match fraction with the first gene than any of the  
17 genes in the cluster have with the first gene;

18        programmed means for repeating the removing step until all  
19 genes are listed in only one cluster.



1        12. A program product having computer readable code stored on a  
2        recordable media for determining similarity between portions of gene  
3        expression profiles comprising the steps of:

4               programmed means for processing a number of gene expression  
5        profiles with a similar sequences algorithm that is a time and  
6        intensity invariant correlation function to obtain a data set of  
7        gene expression pairs and a match fraction for each pair;

8               programmed means for listing gene expression pairs in clusters  
9        by their match fractions;

10               programmed means for removing a first gene from a first cluster  
11        when the first gene is also in a second cluster which has another  
12        gene with a higher match fraction with the first gene than any of  
13        the genes in the first cluster have with the first gene, but;

14               programmed means for retaining the first gene in the first  
15        cluster and removing the first gene from the second cluster when the  
16        difference between the highest match fraction of the first gene with  
17        a gene in the first cluster and the highest match fraction of the  
18        first gene with a gene in the second cluster is less than a minimum  
19        difference threshold and the number of subsequences represented in  
20        the similar gene pair having the highest match fraction in the first  
21        cluster is higher than the number of subsequences represented in the  
22        similar gene pair having the highest match fraction in the second  
23        cluster;

24               programmed means for repeating the removing step until all  
25        genes are listed in only one cluster.

1        13. A program product having computer readable code stored on a  
2        recordable media for determining similarity between portions of gene  
3        expression profiles comprising the steps of:

4               programmed means for processing a number of gene expression  
5        profiles with a similar sequences algorithm that is a time and  
6        intensity invariant correlation function to obtain a data set of  
7        gene expression pairs and a match fraction for each pair;

8               programmed means for choosing a threshold match fraction;

9               programmed means for listing gene expression pairs in clusters  
10       by their match fractions above the threshold;

11              programmed means for adding each gene not already in a cluster  
12       to a cluster having another gene having a highest match fraction  
13       with the each gene without regard of the threshold;

14              programmed means for removing a first gene from a cluster when  
15       the first gene is also in another cluster which has another gene  
16       with a higher match fraction with the first gene than any of the  
17       genes in the cluster have with the first gene;

18              programmed means for repeating the removing step until all  
19       genes are listed in only one cluster.

1        14. A program product having computer readable code stored on a  
2 recordable media for determining similarity between portions of gene  
3 expression profiles comprising the steps of:

4        programmed means for processing a number of gene expression  
5 profiles with a similar sequences algorithm that is a time and  
6 intensity invariant correlation function to obtain a data set of  
7 gene expression pairs and a match fraction for each pair;

8        programmed means for choosing a threshold match fraction;

9        programmed means for listing gene expression pairs in clusters  
10 by their match fractions above the threshold;

11       programmed means for adding each gene not already in a cluster  
12 to a cluster having another gene having a highest match fraction  
13 disregarding the threshold with the each gene;

14       programmed means for removing a first gene from a first cluster  
15 when the first gene is also in a second cluster which has another  
16 gene with a higher match fraction with the first gene than any of  
17 the genes in the first cluster have with the first gene, but;

18       programmed means for retaining the first gene in the first  
19 cluster and removing the first gene from the second cluster when the  
20 difference between the highest match fraction of the first gene with  
21 a gene in the first cluster and the highest match fraction of the  
22 first gene with a gene in the second cluster is less than a minimum  
23 difference threshold and the number of subsequences represented in  
24 the similar gene pair having the highest match fraction in the first  
25 cluster is higher than the number of subsequences represented in the  
26 similar gene pair having the highest match fraction in the second  
27 cluster;

28       programmed means for repeating the removing and retaining steps  
29 until all genes are listed in only one cluster.

1        15. A program product having computer readable code stored on a  
2        recordable media for determining similarity between genes comprising  
3        the steps of:

4            programmed means for listing genes to be compared by their gene  
5        expression profiles;

6            programmed means for processing the listed gene expression  
7        profiles with a similar sequences algorithm that is a time and  
8        intensity invariant correlation function to obtain a data set of  
9        gene expression pairs and a match fraction for each pair;

10          programmed means for choosing a threshold match fraction;

11          programmed means for creating a null set  $G(0)$  to hold genes  
12        accounted for;

13          programmed means for assigning genes  $i$  and  $j$  to cluster 1 if  
14        they have a match fraction greater than the threshold;

15          programmed means for assigning gene  $k$  to cluster 1 if it has a  
16        match fraction greater than the threshold with either gene  $i$  or gene  
17         $j$ ;

18          programmed means for assigning genes  $k$  and  $l$  to cluster 2 if  
19        they have a match fraction greater than the threshold and if both  
20        gene  $k$  and gene  $l$  do not have match fractions above the threshold  
21        with either gene  $i$  or gene  $j$ ;

22          programmed means for removing a first gene from a cluster when  
23        another cluster has another gene with a higher match fraction with  
24        the first gene;

25          programmed means for repeating the removing step until all  
26        genes are listed in only one cluster.  
27

1        16. A program product having computer readable code stored on a  
2 recordable media for determining similarity between genes comprising  
3 the steps of:

4        programmed means for listing genes to be compared by their gene  
5 expression profiles;

6        programmed means for processing the listed gene expression  
7 profiles with a similar sequences algorithm that is a time and  
8 intensity invariant correlation function to obtain a data set of  
9 gene expression pairs and a match fraction for each pair;

10       programmed means for choosing a threshold match fraction;

11       programmed means for creating a null set  $G(0)$  to hold genes  
12 accounted for;

13       programmed means for assigning genes  $i$  and  $j$  to cluster 1 if  
14 they have a match fraction greater than the threshold;

15       programmed means for assigning gene  $k$  to cluster 1 if it has a  
16 match fraction greater than the threshold with either gene  $i$  or gene  
17  $j$ ;

18       programmed means for assigning genes  $k$  and  $l$  to cluster 2 if  
19 they have a match fraction greater than the threshold and if both  
20 gene  $k$  and gene  $l$  do not have match fractions above the threshold  
21 with either gene  $i$  or gene  $j$ ;

22       programmed means for removing a first gene from a cluster when  
23 another cluster has another gene with a higher match fraction with  
24 the first gene, unless the another gene requires a larger number of  
25 subsequences to achieve similarity with the first gene;

26       programmed means for repeating the removing step until all  
27 genes are listed in only one cluster.  
28

1        20. In a method of determining similarity between portions of  
2 gene expression profiles which includes processing a number of gene  
3 expression profiles using a computer with a similar sequences  
4 algorithm that is a time and intensity invariant correlation  
5 function to obtain a data set of gene expression pairs and a match  
6 fraction for each pair, the improvement comprising the steps of:

7        listing gene expression pairs in clusters by their match  
8 fractions;

9        removing a first gene from a cluster when another cluster has  
10 another gene with a higher match fraction with the first gene,  
11 unless the another gene requires a larger number of subsequences to  
12 achieve similarity with the first gene;

13        repeating the removing step until all genes are listed in only  
14 one cluster;

15        providing output of the listing of clusters of gene  
16 expression profiles.

1           **(IX) Evidence Appendix**

2           No evidence is being submitted in this appeal.

3

1           **(X) Related Proceedings Appendix**

2           None.